

inactivating said DNA mismatch repair system of said
plant cell.

D⁶
[Please **add** new claim 44 as follows:]

44. (NEW) The process of claim 43, wherein said plant is selected from the group consisting of Brassicaceae, Poaceae, Solanaceae, Asteraceae, Malvaceae, Fabaceae, Linaceae, Canabinaceae, Dauaceae and Cucurbitaceae.
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IN THE SPECIFICATION

Please **delete** the Sequence Listing of record and **substitute therefor**, the Second Substitute Sequence Listing attached hereto in paper and computer-readable form.

Please **amend** the abstract with the following rewritten abstract:

D⁸
(AMENDED) The present invention relates to an isolated and purified DNA comprising a nucleotide sequence that encodes a polypeptide functionally involved in the DNA mismatch repair system of a plant.

Please **amend** the paragraph beginning at page 12, line 34 and ending at page 13,

line 4 with the following rewritten paragraph:

29 (AMENDED) Primers UPMU and DOMU correspond to conserve amino acid sequences of the proteins MutS (*E. coli* and *S. typhimurium*), HexA (*S. pneumoniae*), Repl (mouse) and Ducl (human). The conserved regions to which they are targeted are TGPNM (SEQ ID NO:99) for UPMU and FATHY (SEQ ID NO:100) or FVTHY (SEQ ID NO:101) for DOMU. These primers have been used to isolate MSH2 and MSH1 from yeast (Reenan and Kolodner, Genetics 132:963-973 (1992)) and MSH2 from *Xenopus* and mouse (Varlet et al., *Nucleic Acids Res.* 22:5723-5728 (1994)).